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0102

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## RAW SEQUENCE LISTING

DATE: 12/28/2001

PATENT APPLICATION: US/09/942,936

TIME: 16:06:16

Input Set : A:\032301.205.seq.ST25.txt

Output Set: N:\CRF3\12282001\I942936.raw

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3 <110> APPLICANT: BATHE, Brigitte  
 5 <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE sigh GENE  
 7 <130> FILE REFERENCE: 032301 WD 295  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/942,936  
 C--> 9 <141> CURRENT FILING DATE: 2001-08-31  
 9 <160> NUMBER OF SEQ ID NOS: 4  
 11 <170> SOFTWARE: PatentIn version 3.1  
 13 <210> SEQ ID NO: 1  
 14 <211> LENGTH: 1148  
 15 <212> TYPE: DNA  
 16 <213> ORGANISM: Corynebacterium glutamicum  
 18 <220> FEATURE:  
 19 <221> NAME/KEY: CDS  
 20 <222> LOCATION: (302)..(919)  
 21 <223> OTHER INFORMATION:  
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 27 aggtcacggc gattagtctc aacaatttcg gtgcttaaag gatcctgcgg attattgacg 120  
 29 gtgaagtaga acattgtttc cccctagatt tgaagtggta catatgttct aactgatgtg 180  
 31 gtggacacgc gggggtagag taaagtctaa gcaacagctc acgtggcttt acagctaccc 240  
 33 ccgaaaggctc tgttttttat cggaagtaga atagtcaaca cgcattttcg aaaggggcca 300  
 35 c atg gct gaa aac cga acc ggc aca gtc gat gga gac gcg ttg gct gcc 349  
 36 Met Ala Glu Asn Arg Thr Gly Thr Val Asp Gly Asp Ala Leu Ala Ala  
 37 1 5 10 15  
 39 cgc ttt gaa gag gag gca ctg cca ctc ctt gac cag ctc tat ggc ggt 397  
 40 Arg Phe Glu Glu Glu Ala Leu Pro Leu Leu Asp Gln Leu Tyr Gly Gly  
 41 20 25 30  
 43 gct ctg cgc atg act aga aat ccc gca gat gcg gaa gat ctc gtg caa 445  
 44 Ala Leu Arg Met Thr Arg Asn Pro Ala Asp Ala Glu Asp Leu Val Gln  
 45 35 40 45  
 47 gac acc tat atc aag gcg tac cag gcg ttc gcg agc ttc aaa cca ggc 493  
 48 Asp Thr Tyr Ile Lys Ala Tyr Gln Ala Phe Ala Ser Phe Lys Pro Gly  
 49 50 55 60  
 51 acc aac ctg aag gct tgg ctc tat cgg atc atg acg aat acc tac atc 541  
 52 Thr Asn Leu Lys Ala Trp Leu Tyr Arg Ile Met Thr Asn Thr Tyr Ile  
 53 65 70 75 80  
 55 aac atg tac cga aag aaa cag agg cag cca tcg caa acc tct gcc gat 589  
 56 Asn Met Tyr Arg Lys Lys Gln Arg Gln Pro Ser Gln Thr Ser Ala Asp  
 57 85 90 95  
 59 gag atc act gac tac cag ctc gtt gaa tct caa tcg cat acc tca aca 637  
 60 Glu Ile Thr Asp Tyr Gln Leu Val Glu Ser Gln Ser His Thr Ser Thr  
 61 100 105 110  
 63 ggg ctg gaa tcc gcc gag gtt gag gct ctg aaa aat ctg cca gac gga 685  
 64 Gly Leu Glu Ser Ala Glu Val Glu Ala Leu Lys Asn Leu Pro Asp Gly  
 65 115 120 125  
 67 aaa att ggc gat gca atg aat caa ctc agc ccg gaa tac cgg atg gtg 733  
 68 Lys Ile Gly Asp Ala Met Asn Gln Leu Ser Pro Glu Tyr Arg Met Val

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69      130      135      140
71 gtt tat tat gcc gat gta gaa gat ctc gca tac aaa gaa atc gcc gag      781
72 Val Tyr Tyr Ala Asp Val Glu Asp Leu Ala Tyr Lys Glu Ile Ala Glu
73 145      150      155      160
75 atc atg gac gtt cca ctc gga act gtg atg tcc cga ctc cat cgt gga      829
76 Ile Met Asp Val Pro Leu Gly Thr Val Met Ser Arg Leu His Arg Gly
77      165      170      175
79 aga aaa cag ctc cga gga atg tta aag gaa gta gcg aag gaa caa ggc      877
80 Arg Lys Gln Leu Arg Gly Met Leu Lys Glu Val Ala Lys Glu Gln Gly
81      180      185      190
83 att ggt ctt gaa cat ccc gac atg aag aaa aat tcg gag gca      919
84 Ile Gly Leu Glu His Pro Asp Met Lys Lys Asn Ser Glu Ala
85      195      200      205
87 taacgatgac gaatctcaac cgcagcgact cgcaagggtga ttgtggctgc cctgaattct      979
89 tcgatgaaat gtatcagcta ctgcacgatc aactcagcga gtccgcctgc gagcgtctgc      1039
91 ggattcacgc ggcaggctgc ccggcatgcc agcaactgct agaggccgaa tcggagtttc      1099
93 gtagtctgtt gcgcaagtgc tgctgcgaat cggcacctgt ggagctccg      1148
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97 <211> LENGTH: 206
98 <212> TYPE: PRT
99 <213> ORGANISM: Corynebacterium glutamicum
101 <400> SEQUENCE: 2
103 Met Ala Glu Asn Arg Thr Gly Thr Val Asp Gly Asp Ala Leu Ala Ala
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107 Arg Phe Glu Glu Glu Ala Leu Pro Leu Leu Asp Gln Leu Tyr Gly Gly
108      20      25      30
111 Ala Leu Arg Met Thr Arg Asn Pro Ala Asp Ala Glu Asp Leu Val Gln
112      35      40      45
115 Asp Thr Tyr Ile Lys Ala Tyr Gln Ala Phe Ala Ser Phe Lys Pro Gly
116      50      55      60
119 Thr Asn Leu Lys Ala Trp Leu Tyr Arg Ile Met Thr Asn Thr Tyr Ile
120 65      70      75      80
123 Asn Met Tyr Arg Lys Lys Gln Arg Gln Pro Ser Gln Thr Ser Ala Asp
124      85      90      95
127 Glu Ile Thr Asp Tyr Gln Leu Val Glu Ser Gln Ser His Thr Ser Thr
128      100      105      110
131 Gly Leu Glu Ser Ala Glu Val Glu Ala Leu Lys Asn Leu Pro Asp Gly
132      115      120      125
135 Lys Ile Gly Asp Ala Met Asn Gln Leu Ser Pro Glu Tyr Arg Met Val
136      130      135      140
139 Val Tyr Tyr Ala Asp Val Glu Asp Leu Ala Tyr Lys Glu Ile Ala Glu
140 145      150      155      160
143 Ile Met Asp Val Pro Leu Gly Thr Val Met Ser Arg Leu His Arg Gly
144      165      170      175
147 Arg Lys Gln Leu Arg Gly Met Leu Lys Glu Val Ala Lys Glu Gln Gly
148      180      185      190
151 Ile Gly Leu Glu His Pro Asp Met Lys Lys Asn Ser Glu Ala
152      195      200      205
155 <210> SEQ ID NO: 3

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156 <211> LENGTH: 28  
157 <212> TYPE: DNA  
158 <213> ORGANISM: Corynebacterium glutamicum  
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164 <210> SEQ ID NO: 4  
165 <211> LENGTH: 28  
166 <212> TYPE: DNA  
167 <213> ORGANISM: Corynebacterium glutamicum  
169 <400> SEQUENCE: 4  
170 tgtctagaaa gaattcaggg cagccaca 28

VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date